(c) expressing the modified nucleic acid in a host cell to produce the variant alpha-amylase,

wherein the variant has alpha-amylase enzymatic activity and has at least one altered property relative to the parent.--

REMARKS

Entry of this amendment is respectfully requested, as it is believed to place the claims in condition for allowance and would not require further search.

Reconsideration and allowance are respectfully requested.

Claims 71-75 were pending. In this response, claims 72-75 are cancelled without prejudice; claim 71 is amended for further clarity; and new claims 76-78 are added. Support for the amendments and new claims can be found in the specification and claims as originally filed. For example, designing α-amylase variants by identifying mutation targets in a three-dimensional structure is disclosed, e.g., in Example 1. The location of domain B within the sequence of SEQ ID NO:2 is disclosed at page 8, lines 1-2. The residues identified as being part of a substrate-binding site are disclosed at page 10, line 30 - page 11, line 2. No new matter is added. Accordingly, claims 71 and 76-78 are pending and at issue.

Rejection Under 35 U.S.C. §112, First Paragraph

Claims 71-75 have been rejected under 35 U.S.C. §112, first paragraph, for lack of enablement. The Examiner contends that obtaining X-ray crystallographic structures is unpredictable, and that it would require undue experimentation to obtain such structures from α-amylases that are 70% homologous to the polypeptide whose X-ray structure is disclosed in the Appendix. This rejection is respectfully traversed.

In this response, claim 71 has been amended so that it does not require obtaining an X-ray crystallographic structure from any α-amylase other than the one whose X-ray structure is depicted in Appendix 1 of the present application.

The high degree of structural relatedness between the members of the family of α-amylases designated "Termamyl-like" in the present specification, (i.e., those which have sequences at least 70% homologous to SEQ ID Nos: 2, 4, 6, or 13),

means that one of ordinary skill in the art, based on the X-ray crystallographic structure of Appendix 1, would be able to identify target sites for mutation in *any* member of this enzyme family and thus would be able to practice the full scope of the present claims without undue experimentation. On this basis, it is respectfully submitted that the present claims are fully enabled by the present specification and that this rejection has been overcome.

Rejection Under 35 U.S.C. §112, Second Paragraph

Claim 72 has been rejected under 35 U.S.C. § 112, second paragraph, as indefinite, for the recitation of "an unrelated α-amylase". In this response, claim 72 is cancelled, rendering this rejection moot.

In view of the above amendments and remarks, it is believed that the claims are in condition for allowance, and a determination to that effect is earnestly solicited.

Respectfully submitted,

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